```
 1                           SEQUENCE LISTING
 2
 3
 4
 5   (1)  GENERAL INFORMATION:
 6
 7        (i)  APPLICANT(S):  Kaufman, Randal J.
 8                            Wasley, Louise
 9
10       (ii)  TITLE OF INVENTION:  Method of Increasing Yield of
11                                  Mature Proteins
12
13      (iii)  NUMBER OF SEQUENCES:  2
14
15       (iv)  CORRESPONDENCE ADDRESS:
16
17             (A) ADDRESSEE:  Genetics Institute, Inc.
18             (B) STREET:     87 CambridgePark Drive
19             (C) CITY:       Cambridge
20             (D) STATE:      Massachusetts
21             (E) COUNTRY:    United States of America
22             (F) ZIP:        02140
23
24        (v)  COMPUTER READABLE FORM:
25
26             (A) MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb storage
27
28             (B) COMPUTER:  IBM PS/2
29
30             (C) OPERATING SYSTEM:  PC-DOS
31
32             (D) SOFTWARE:  WordPerfect 5.1
33
34       (vi)  CURRENT APPLICATION DATA:
35
36             (A)  APPLICATION NUMBER: not yet available
37
38             (B)  FILING DATE:  26 November 1990
39
40             (C)  CLASSIFICATION:  not yet available
41
42      (vii)  PRIOR APPLICATION DATA: not applicable
43
44             (A)  APPLICATION NUMBER:
45
46             (B)  FILING DATE:
47
48     (viii)  ATTORNEY/AGENT INFORMATION
49
50             (A) NAME:  Ellen J. Kapinos, Esquire
51             (B) REGISTRATION NUMBER: 32,245
52             (C) REFERENCE/DOCKET NUMBER: GI 5181
53
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54   (ix) TELECOMMUNICATION INFORMATION:
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56   (A)   TELEPHONE: (617) 876-1170
57   (B)   TELEFAX: (617) 876-5851
58
59   (2)   INFORMATION FOR SEQ ID NO:1
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61   (i)   SEQUENCE CHARACTERISTICS:
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63   (A)   LENGTH: 2385 base pairs
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65   (B)   TYPE: nucleic acid
66
67   (C)   STRANDEDNESS: double
68
69   (D)   Topology: unknown
70
71   (ii)   MOLECULE TYPE: partial human genomic DNA
72
73   (A) DESCRIPTION: sequence encoding furin
74
75   (iii)   HYPOTHETICAL: no
76
77   (iv)   ANTI-SENSE: no
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79   (v)   PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,
80   Nucl. Acids. Res., 18:664 (1990)
81
82   (vi)   SEQUENCE DESCRIPTION: SEQ ID NO:1
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84   ATG GAG CTC AGG CCC TGG TTC   21
85   Met Glu Leu Arg Pro Trp Leu
86   1   5
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88   CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA   60
89   Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
90   ·   10   15   20
91
92   GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG   99
93   Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
94   25   30
95
96   TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC   138
97   Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
98   35   40   45
99
100
101 AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG   177
102 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
103   50   55
104
105 ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG   216
106 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val

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107    60                        65                        70
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109
110    ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC    255
111    Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
112        75                        80                        85
113
114
115    CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG    294
116    Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln
117                    90                        95
118
119    CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG    333
120    Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln
121        100                       105                       110
122
123    GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG    372
124    Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu
125                    115                       120
126
127    TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC    411
128    Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala
129    125                       130                       135
130
131    TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC    450
132    Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser
133            140                       145                       150
134
135    ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG    489
136    Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu
137                    155                       160
138
139    GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT    528
140    Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
141        165                       170                       175
142
143    GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG    567
144    Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met
145                    180                       185
146
147    AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG    606
148    Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val
149    190                       195                       200
150
151    GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG    645
152    Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val
153            205                       210                       215
154
155    GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT    684
156    Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp
157                    220                       225
158
159    GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC    723
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160  Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly
161      230             235             240
162
163  CTG AAC CCC AAC CAC ATC CAC ATC TAC AGT GCC AGC TGG      762
164  Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp
165          245             250
166
167  GGC CCC GAG GAT GAC GGC AAG ACA GTG GAT GGG CCA GCC      801
168  Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala
169  255             260             265
170
171  CGG CTC GCC GAG GAG GCC TTC TTC CGT GGG CTT AGC CAG      840
172  Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln
173          270             275             280
174
175  GGC CGA GGG GGG CTG GGC TCC ATC TTT GTC TGG GCC TCG      879
176  Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
177              285             290
178
179  GGG AAC GGG GGG CGG GAA CAT GAC AGC TGC AAC TGC GAC      918
180  Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
181      295             300             305
182
183  GGC TAC ACC AAC AGT ATC TAC ACG CTG TCC ATC AGC AGC      957
184  Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
185              310             315
186
187  GCC ACG CAG TTT GGC AAC GTG CCG TGG TAC AGC GAG GCC      996
188  Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
189  320             325             330
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191  TGC TCG TCC ACA CTG GCC ACG ACC TAC AGC AGT GGC AAC     1035
192  Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
193          335             340             345
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195  CAG AAT GAG AAG CAG ATC GTG ACG ACT GAC TTG CGG CAG     1074
196  Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
197              350             355
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199  AAG TGC ACG GAG TCT CAC ACG GGC ACC TCA GCC TCT GCC     1113
200  Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
201      360             365             370
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203  CCC TTA GCA GCC GGC ATC ATT GCT CTC ACC CTG GAG GCC     1152
204  Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
205          375             380
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207  AAT AAG AAC CTC ACA TGG CGG GAC ATG CAA CAC CTG GTG     1191
208  Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
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211  GTA CAG ACC TCG AAG CCA GCC CAC CTC AAT GCC AAC GAC     1230
212  Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
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215   TGG GCC ACC AAT GGT GTG GGG CGG AAA GTG AGC CAC TCA   1269
216   Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
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219   TAT GGC TAC GGG CTT TTC GAC GCA GGC GCC ATG GTG GCC   1308
220   Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
221       425                   430                   435
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223   CTG GCC CAG AAT TGG ACC ACA GTC GCC CCC CAG CGG AAG   1347
224   Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
225               440                   445
226
227   TGC ATC ATC GAC ATC CTC ACC GAG CCC AAA GAC ATC GGG   1386
228   Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
229   450                   455                   460
230
231   AAA CGG CTC GAC CTC CGG AAC ACC GTG ACC GCG TCC CTG   1425
232   Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
233               465                   470                   475
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235   GGC GAG CCC AAC CAC ATC ACT CGG CTG GAG CAC GCT CAG   1464
236   Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
237                   480                   485
238
239   GCG CGG CTC ACC CTG TCC TAT AAT CGC CGT GGC GAC CTG   1503
240   Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
241       490                   495                   500
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243   GCC ATC CAC CTG GTC AGC CCC ATG GGC ACC CGC TCC ACC   1542
244   Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
245               505                   510
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247   CTG CTG GCA GCC AGG CCA CAT GAC TAC TCC GCA GAT GGG   1581
248   Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
249   515                   520                   525
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251   TTT AAT GAC TGG GCC TTC ATG ACA ACT CAT TCC TGG GAT   1620
252   Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
253               530                   535                   540
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255   GAC GAT CCC TCT GGG GAG TGG GTC CTA GAG ATT GAA AAC   1659
256   Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
257               545                   550
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259   ACC AGC GAA GCC AAC AAC TAT GGG ACG CTG ACC AAC TCC   1698
260   Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
261       555                   560                   565
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263   ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC GGG CTC CCC   1737
264   Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
265               570                   575
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267  GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC  1776
268  Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
269  580             585                 590
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271  AGT CAG GCC TGT GTG GTG TGC GAG GAA GGC TTC TCC CTC  1815
272  Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
273          595                 600                 605
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275  CAC CAG AAG AGC TGT GTC CAG CAC TGC CCT CCA GGC TTC  1854
276  His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
277                  610                 615
278
279  GCC CCC CAA GTC CTC GAT ACG CAC TAT AGC ACC GAG AAT  1893
280  Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
281      620                 625                 630
282
283  GAC GTG GAG ACC ATC CGG GCC AGC GTC TGC GCC CCC TGC  1932
284  Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
285              635                 640
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287  CAC GCC TCA TGT GCC ACA TGC CAG GGG CCG GCC CTG ACA  1971
288  His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
289  645                 650                 655
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291  GAC TGC CTC AGC TGC CCC AGC CAC GCC TCC TTG GAC CCT  2010
292  Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
293          660                 665                 670
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295  GTG GAG CAG ACT TGC TCC CGG CAA AGC CAG AGC AGC CGA  2049
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297              675                 680
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299  GAG TCC CCG CCA CAG CAG CAG CCA CCT CGG CTG CCC CCG  2088
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301      685                 690                 695
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303  GAG GTG GAG GCG GGG CAA CGG CTG CGG GCA GGG CTG CTG  2127
304  Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
305              700                 705
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307  CCC TCA CAC CTG CCT GAG GTG GTG GCC GGC CTC AGC TGC  2166
308  Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
309  710                 715                 720
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311  GCC TTC ATC GTG CTG GTC TTC GTC ACT GTC TTC CTG CTC  2205
312  Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
313          725                 730                 735
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315  CTG CAG CTG CGC TCT GGC TTT AGT TTT CGG GGG GTG AAG  2244
316  Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
317              740                 745
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319  GTG TAC ACC ATG GAC CGT GGC CTC ATC TCC TAC AAG GGG   2283
320  Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
321      750                 755                 760
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323  CTG CCC CCT GAA GCC TGG CAG GAG GAG TGC CCG TCT GAC   2322
324  Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
325              765                 770
326
327  TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT   2361
328  Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
329  775                 780                 785
330
331  ATC AAA GAC CAG AGC GCC CTC TGA                        2385
332  Ile Lys Asp Gln Ser Ala Leu End
333          790
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336  (3)    INFORMATION FOR SEQ ID NO:2
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338         (i)    SEQUENCE CHARACTERISTICS:
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340                (A)   LENGTH: 794 amino acids
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342                (B)   TYPE:   amino acids
343
344                (C)   STRANDEDNESS:   single
345
346                (D)   Topology:   unknown
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348         (ii)   MOLECULE TYPE: furin
349
350        (iii)   HYPOTHETICAL:   no
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352        (iv)   ANTI-SENSE:   no
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354         (v)    PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,
355                                 Nucl. Acids. Res., 18:664 (1990)
356
357        (vi)    SEQUENCE DESCRIPTION:   SEQ ID NO:2
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360  Met Glu Leu Arg Pro Trp Leu
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363  Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
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366  Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
367                  25                  30
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369  Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
370       35                  40                  45
371
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372	Ser	Val	Ala	Arg	Lys	His	Gly	Phe	Leu	Asn	Leu	Gly	Gln
373				50					55			
374												
375	Ile	Phe	Gly	Asp	Tyr	Tyr	His	Phe	Trp	His	Arg	Gly	Val
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383				90					95			
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385	Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln
386		100					105					110	
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388	Glu	Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu
389				115					120			
390												
391	Ser	Gly	Val	Thr	Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala
392	125					130					135		
393												
394	Trp	Ala	Gln	Gly	Tyr	Thr	Gly	His	Gly	Ile	Val	Val	Ser
395			140					145					150
396												
397	Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	Pro	Asp	Leu
398				155					160			
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400	Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	Asp	Val	Asn
401		165					170					175	
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403	Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met
404				180					185			
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406	Asn	Asp	Asn	Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val
407	190					195					200		
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409	Ala	Ala	Val	Ala	Asn	Asn	Gly	Val	Cys	Gly	Val	Gly	Val
410			205					210					215
411												
412	Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	Arg	Met	Leu	Asp
413				220					225			
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415	Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	Gly
416		230					235					240	
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418	Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp
419				245					250			
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421	Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala
422	255					260					265		
423												
424	Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln

Patent Application US 07/621,092

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425           270                   275                   280
426
427   Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
428                   285                   290
429
430   Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
431       295                   300                   305
432
433   Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
434               310                   315
435
436
437   Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
438   320               325                   330
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440   Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
441           335                   340                   345
442
443   Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
444               350                   355
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446   Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
447       360                   365                   370
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449   Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
450               375                   380
451
452   Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
453   385               390                   395
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459               415                   420
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461   Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
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464   Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
465               440                   445
466
467   Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
468   450               455                   460
469
470   Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
471       465                   470                   475
472
473   Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
474               480                   485
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476   Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
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479  Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
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482  Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
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485  Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
486          530             535             540
487
488  Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
489              545             550
490
491  Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
492      555             560             565
493
494  Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
495              570             575
496
497  Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
498  580             585             590
499
500  Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
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502
503  His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
504              610             615
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506  Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
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509  Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
510              635             640
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512  His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
513  645             650             655
514
515  Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
516      660             665                 670
517
518  Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
519              675             680
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521  Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
522      685             690                 695
523
524  Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
525              700             705
526
527  Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
528  710             715             720
529
530  Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
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Patent Application US 07/621,092

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531              725                    730                    735
532
533  Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
534                  740                    745
535
536  Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
537      750                    755                    760
538
539  Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
540                  765                    770
541
542  Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
543  775                    780                    785
544
545
546  Ile Lys Asp Gln Ser Ala Leu End
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SEQUENCE VERIFICATION REPORT

Patent Application US 07/621,092

Line	Error	Original text
5	Unknown or Misplaced Identifier	(1). GENERAL INFORMATION:
7	Unknown or Misplaced Identifier	(i) APPLICANT(S): Kaufman, Randal J.
8	Unknown or Misplaced Identifier	Wasley, Louise
10	Unknown or Misplaced Identifier	(ii) TITLE OF INVENTION: Method of Increasing
11	Unknown or Misplaced Identifier	Mature Proteins
13	Unknown or Misplaced Identifier	(iii) NUMBER OF SEQUENCES: 2
15	Unknown or Misplaced Identifier	(iv) CORRESPONDENCE ADDRESS:
17	Unknown or Misplaced Identifier	(A) ADDRESSEE: Genetics Institute, Inc.
18	Unknown or Misplaced Identifier	(B) STREET: 87 CambridgePark Drive
19	Unknown or Misplaced Identifier	(C) CITY: Cambridge
20	Unknown or Misplaced Identifier	(D) STATE: Massachusetts
21	Unknown or Misplaced Identifier	(E) COUNTRY: United States of America
22	Unknown or Misplaced Identifier	(F) ZIP: 02140
24	Unknown or Misplaced Identifier	(v) COMPUTER READABLE FORM:
26	Unknown or Misplaced Identifier	(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
28	Unknown or Misplaced Identifier	(B) COMPUTER: IBM PS/2
30	Unknown or Misplaced Identifier	(C) OPERATING SYSTEM: PC-DOS
32	Unknown or Misplaced Identifier	(D) SOFTWARE: WordPerfect 5.1
34	Unknown or Misplaced Identifier	(vi) CURRENT APPLICATION DATA:
36	Unknown or Misplaced Identifier	(A) APPLICATION NUMBER: not yet available
38	Unknown or Misplaced Identifier	(B) FILING DATE: 26 November 1990
40	Unknown or Misplaced Identifier	(C) CLASSIFICATION: not yet available
42	Unknown or Misplaced Identifier	(vii) PRIOR APPLICATION DATA: not applicable
44	Unknown or Misplaced Identifier	(A) APPLICATION NUMBER:
46	Unknown or Misplaced Identifier	(B) FILING DATE:
48	Unknown or Misplaced Identifier	(viii) ATTORNEY/AGENT INFORMATION
50	Unknown or Misplaced Identifier	(A) NAME: Ellen J. Kapinos, Esquire
51	Unknown or Misplaced Identifier	(B) REGISTRATION NUMBER: 32,245
52	Unknown or Misplaced Identifier	(C) REFERENCE/DOCKET NUMBER: GI 5181
54	Unknown or Misplaced Identifier	(ix) TELECOMMUNICATION INFORMATION:
56	Unknown or Misplaced Identifier	(A) TELEPHONE: (617) 876-1170
57	Unknown or Misplaced Identifier	(B) TELEFAX: (617) 876-5851
80	Extra Level-0 Records	Nucl. Acids. Res., 18:664 (1990)
355	Extra Level-0 Records	Nucl. Acids. Res., 18:664 (1990)
546	Wrong Amino Acid Designator	Ile Lys Asp Gln Ser Ala Leu End

Manditory Identifier that was not found
GENERAL INFORMATION
APPLICANT
TITLE OF INVENTION
NUMBER OF SEQUENCES
CORRESPONDENCE ADDRESS
ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
COMPUTER READABLE FORM
MEDIUM TYPE
COMPUTER
OPERATING SYSTEM
SOFTWARE
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE